

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/445,258

DATE: 07/16/2001

TIME: 11:37:50

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\07162001\I445258.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Kato, Seishi
 5 Sekine, Shingo
 6 Kimura, Tomoko
 8 <120> TITLE OF INVENTION: HUMAN PROTEINS HAVING TRANSMEMBRANE
 9 DOMAINS AND DNAs ENCODING THESE PROTEINS
 13 <130> FILE REFERENCE: GIN-6706CPUS
 15 <140> CURRENT APPLICATION NUMBER: 09/445,258
 16 <141> CURRENT FILING DATE: 1999-12-01
 18 <150> PRIOR APPLICATION NUMBER: PCT/US98/02445
 19 <151> PRIOR FILING DATE: 1998-06-03
 21 <150> PRIOR APPLICATION NUMBER: JP 9-144948
 22 <151> PRIOR FILING DATE: 1997-06-03
 24 <160> NUMBER OF SEQ ID NOS: 54
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0

ERRORED SEQUENCES

2501 <210> SEQ ID NO: 54
 2502 <211> LENGTH: 1914
 2503 <212> TYPE: DNA
 2504 <213> ORGANISM: Homo sapiens
 2506 <220> FEATURE:
 2507 <221> NAME/KEY: CDS
 2508 <222> LOCATION: (80)...(661)
 2510 <400> SEQUENCE: 54
 2511 actctctgtct gtcgcccgtc ccgcgcgtc ctccgaccgc ctccgctccg ctccgctcgg 60
 2512 ccccgcgccg cccgtcaac atg atc cgc tgc gcc ctg gcc tgc gag cgc tgc 112
 2513 Met Ile Arg Cys Gly Leu Ala Cys Glu Arg Cys
 2514 1 5 10
 2516 cgc tgg atc ctg ccc ctg ctc cta ctc agc gcc atc gcc ttc gac atc 160
 2517 Arg Trp Ile Leu Pro Leu Leu Leu Ser Ala Ile Ala Phe Asp Ile
 2518 15 20 25
 2520 atc gcg ctg gcc gcc cgc gcc tgg ttg cag tct agc gac cac gcc cag 208
 2521 Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser Ser Asp His Gly Gln
 2522 30 35 40
 2524 acg tcc tcg ctg tgg tgg aaa tgc tcc caa gag gcc gcc gcc agc ggg 256
 2525 Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu Gly Gly Gly Ser Gly
 2526 45 50 55
 2528 tcc tac gag gag gcc tgt cag agc ctc atg gag tac gcg tgg ggt aga 304
 2529 Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu Tyr Ala Trp Gly Arg
 2530 60 65 70 75
 2532 gca gcg gct gcc atg ctc ttc tgt gcc ttc atc atc ctg gtg atc tgt 352
 2533 Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile Ile Leu Val Ile Cys
 2534 80 85 90
 2536 ttc atc ctc tcc ttc ttc gcc ctc tgt gga ccc cag atg ctt gtc ttc 400
 2537 Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro Gln Met Leu Val Phe

RAW SEQUENCE LISTING

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```

2538          95          100          105
2540 ctg aga gtg att gga ggt ctc ctt gcc ttg gct gct gtg ttc cag atc 448
2541 Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala Ala Val Phe Gln Ile
2542          110          115          120
2544 atc tcc ctg gta att tac ccc gtg aag tac acc cag acc ttc acc ctt 496
2545 Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr Gln Thr Phe Thr Leu
2546          125          130          135
2548 cat gcc aac cgt gct gtc act tac atc tat aac tgg gcc tac ggc ttt 544
2549 His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn Trp Ala Tyr Gly Phe
2550 140          145          150          155
2552 ggg tgg gca gcc acg att atc ctg atc ggc tgt gcc ttc ttc ttc tgc 592
2553 Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys Ala Phe Phe Phe Cys
2554          160          165          170
2556 tgc ctc ccc aac tac gaa gat gac ctt ctg ggc aat gcc aag ccc agg 640
2557 Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly Asn Ala Lys Pro Arg
2558          175          180          185
2560 tac ttc tac aca tct gcc taa cttgggaatg aatgtgggag aaaatcgctg 691
2561 Tyr Phe Tyr Thr Ser Ala *
2562          190
2564 ctgctgagat ggactccaga agaagaaact gtttctccag gcgactttga acccattttt 751
2565 tggcagtgtt catattatta aactagtcaa ataagctaaa ataatttggg agaaaatatt 811
2566 ttttaagtag tgttatagtt tcatgtttat cttttattat gttttgtgaa gttgtgtctt 871
2567 ttcactaatt acctatacta tgccaatatt tccttatatc tatccataac atttatacta 931
2568 catttgtaag agaatatgca cgtgaaactt aacactttat aaggtaaaaa tgaggtttcc 991
2569 aagatttaaat aatctgatca agttcttggt atttccaaat agaatggact tggctgtgta 1051
2570 agggctaagg agaagaggaa gataagggtta aaagttgtta atgaccaaac attctaaaag 1111
2571 aaatgcaaaa aaaaagttaa ttttcaagcc ttcgaactat ttaaggaaag caaaatcatt 1171
2572 tcctaaatgc atatcatttg tgagaatttc tcattaatat cctgaatcat tcatttcagc 1231
2573 taaggcttca tgttgactcg atatgtcatc taggaaagta ctatttcatg gtccaaacct 1291
2574 gttgccatag ttggttaaggc tttcctttaa gtgtgaaata tttagatgaa attttctctt 1351
2575 ttaaagttct ttatagggtt aggggtgtggg aaaatgctat attaataaat ctgtagtgtt 1411
2576 ttgtgtttat atgttcagaa ccagagtaga ctggattgaa agatggactg ggtctaattt 1471
2577 atcatgactg atagatctgg ttaagttgtg tagtaaagca ttaggagggt cattcttgtc 1531
2578 acaaaagtgc cactaaaaca gcctcaggag aataaatgac ttgcttttct aaatctcagg 1591
2579 tttatctggg ctctatcata tagacaggct tctgatagtt tgcaactgta agcagaaacc 1651
2580 tacatatagt taaaatcctg gtctttcttg gtaaacagat tttaaatgtc tgatataaaa 1711
2581 catgccacag gagaattcgg ggatttgagt ttctctgaat agcatatata tgatgcatcg 1771
2582 gataggatcat tatgattttt taccatttcg acttacataa tgaaaaccaa ttcattttta 1831
2583 atatcagatt attattttgt aagttgtgga aaaagctaata tgtagttttc attatgaagt 1891
2584 tttcccaata aaccaggat tct 1914

```

E--> 2585 gln-6706cPus 9*delete*

VERIFICATION SUMMARY

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L:2585 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:54
L:2585 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:54
L:2585 M:254 E: No. of Bases conflict, LENGTH:Input:9 Counted:1922 SEQ:54
L:2585 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:7
L:2585 M:112 C: (48) String data converted to lower case,
L:2585 M:252 E: No. of Seq. differs, <211>LENGTH:Input:1914 Found:1922 SEQ:54